

ALIGNMENT #4

```

Qy      368 HisGlnLysGlyLysAspGluGlyValValTyrSerValValHisArgThrSerLysArg 387
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 CACCAGAAAGGGAAAGATGAAGGTGTTGTCTACTCTGTGGTGCATAGAACCTCAAAGAGG 1140

Qy      388 SerGluAlaArgSerAlaGluPheThrValGlyArgLysAspSerSerIleIleCysAla 407
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 AGTGAAGCCAGGTCTGCTGAGTTCACCGTGGGAGAAAGGACAGTTCTATCATCTGTGCG 1200

Qy      408 GluValArgCysLeuGlnProSerGluValSerSerThrGluValAsnMetArgSerArg 427
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 GAGGTGAGATGCCTGCAGCCCAGTGAGGTTTCATCCACGGAGGTGAATATGAGAAGCAGG 1260

Qy      428 ThrLeuGlnGluProLeuSerAspCysGluGluValLeuCys 441
          ||||||||||||||||||||||||||||||||||||||||
Db      1261 ACTCTCCAAGAACCCTTAGCGACTGTGAGGAGGTTCTCTGC 1302

```

RESULT 5

DJ447641

LOCUS DJ447641 1997 bp DNA linear PAT 10-JUL-2008

DEFINITION A novel immunosuppressive receptor.

ACCESSION DJ447641

VERSION DJ447641.1 GI:194091312

KEYWORDS JP 2004208583-A/2.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1997)

AUTHORS Takahashi,T., Manabe,T., Isogai,T., Sugiyama,T., Irie,R.,
Wakamatsu,A., Ishii,S. and Sato,H.

TITLE A novel immunosuppressive receptor

JOURNAL Patent: JP 2004208583-A 2 29-JUL-2004;
Mochida Pharmaceutical Co Ltd, Research Association for
Biotechnology

COMMENT OS homo sapiens

PN JP 2004208583-A/2

PD 29-JUL-2004

PF 27-DEC-2002 JP 2002381558

PI tomohiro takahashi,tadashi manabe,takao isogai,tomoyasu PI
sugiyama,

PI ryotaro irie,ai wakamatsu,shizuko ishii,hiroyuki sato CC

FH Key Location/Qualifiers.

FEATURES Location/Qualifiers

source 1..1997

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Length:	1997		
Score:	2302.00	Matches:	438
Percent Similarity:	99.3%	Conservative:	1
Best Local Similarity:	99.1%	Mismatches:	0
Query Match:	98.4%	Indels:	3
DB:	9	Gaps:	1

US-10-574-045-4 (1-441) x DJ447641 (1-1997)

Qy	1	MetLeuProSerLeuGlyProMetLeuLeuTrpThrAlaValLeuLeuPheValProCys	20
Db	87	ATGTTGCCATCTTTAGCCCCATGCTGCTCTGGACGGCTGTGCTGCTCTTTGTTCCCTGT	146
Qy	21	ValGlyLysThrValTrpLeuTyrLeuGlnAlaTrpProAsnProValPheGluGlyAsp	40
Db	147	GTTGGAAACTGTCTGGCTGTACCTCCAAGCCTGGCCAAACCTGTGTTGAAGGAGAT	206
Qy	41	AlaLeuThrLeuArgCysGlnGlyTrpLysAsnThrProLeuSerGlnValLysPheTyr	60
Db	207	GCCCTGACTCTGCCATGTCAGGGATGGAAGAATACACCACTGTCTCAGTGAAGTTCTAC	266
Qy	61	ArgAspGlyLysPheLeuHisPheSerLysGluAsnGlnThrLeuSerMetGlyAlaAla	80
Db	267	AGAGATGGAAATTCCTTCATTCTCTAAGGAAACCAGACTCTGCCATGGGAGCAGCA	326
Qy	81	ThrValGlnSerArgGlyGlnTyrSerCysSerGlyGlnValMetTyrIleProGlnThr	100
Db	327	ACAGTGCAGAGCCGTGGCCAGTACAGCTGCTCTGGGCAGGTGATGTATATCCACAGACA	386
Qy	101	PheThrGlnThrSerGluThrAlaMetValGlnValGlnGluLeuPheProProProVal	120
Db	387	TTCACACAACTTCAGAGACTGCCATGGTTCAAGTCCAAGAGCTGTTCCACCTCCTGTG	446
Qy	121	LeuSerAlaIleProSerProGluProArgGluGlySerLeuValThrLeuArgCysGln	140
Db	447	CTGAGTGCCATCCCTCTCCTGAGCCCCGAGAGGGTAGCCTGGTGACCCTGAGATGTCAG	506
Qy	141	ThrLysLeuHisProLeuArgSerAlaLeuArgLeuLeuPheSerPheHisLysAspGly	160
Db	507	ACAAAGCTGCACCCCTGAGGTCAGCCTTGAGGCTCCTTTCTCCTCCACAAGGACGGC	566
Qy	161	HisThrLeuGlnAspArgGlyProHisProGluLeuCysIleProGlyAlaLysGluGly	180
Db	567	CACACCTTGAGGACAGGGCCCTCACCAGAACTCTGCATCCCGGAGCCAAGGAGGGA	626
Qy	181	AspSerGlyLeuTyrTrpCysGluValAlaProGluGlyGlyGlnValGlnLysGlnSer	200
Db	627	GACTCTGGGCTTTACTGGTGTGAGGTGGCCCTGAGGGTGGCCAGGTCCAGAAGCAGAGC	686
Qy	201	ProGlnLeuGluValArgValGlnAlaProValSerArgProValLeuThrLeuHisHis	220
Db	687	CCCCAGCTGGAGGTCAGAGTGCAGGCTCCTGTATCCCGTCTGTGCTCACTCTGCACCAC	746

Qy	221	GlyProAlaAspProAlaValGlyAspMetValGlnLeuLeuCysGluAlaGlnArgGly	240
Db	747	GGGCCTGCTGACCCTGCTGTGGGGACATGGTGCAGCTCCTCTGTGAGGCACAGAGGGGC	806
Qy	241	SerProProIleLeuTyrSerPheTyrLeuAspGluLysIleValGlyAsnHisSerAla	260
Db	807	TCCCCTCCGATCCTGTATTCCTTCTACCTTGATGAGAAGATTGTGGGGAACCACTCAGCT	866
Qy	261	ProCysGlyGlyThrThrSerLeuLeuPheProValLysSerGluGlnAspAlaGlyAsn	280
Db	867	CCCTGTGGTGAACCACTCCCTCCTCTCCAGTGAAGTCAGAACAGGATGCTGGGAAC	926
Qy	281	TyrSerCysGluAlaGluAsnSerValSerArgGluArgSerGluProLysLysLeuSer	300
Db	927	TACTCTGCGAGGCTGAGAACAGTGTCTCCAGAGAGAGAGTGGAGCCCAAGAGCTGTCT	986
Qy	301	LeuLysGlySerGlnValLeuPheThrProAlaSerAsnTrpLeuValProTrpLeuPro	320
Db	987	CTGAAGGGTTCTCAAGTCTTGTTACTCCCGCCAGCAACTGGCTGGTTCTTGCTTCCT	1046
Qy	321	AlaSerLeuLeuGlyLeuMetValIleAlaAlaAlaLeuLeuValTyrValArgSerTrp	340
Db	1047	GCGAGCCTGCTTGGCCTGATGGTTATTGTGCTGCACCTCTGGTTTATGTGAGATCCTGG	1106
Qy	341	ArgLysAlaGlyProLeuProSerGlnIleProProThrAlaProGlyGlyGluGlnCys	360
Db	1107	AGAAAAGCTGGGCCCCTTCCATCCCAGATACCACCCACAGCTCCAGGTGGAGAGCAGTGC	1166
Qy	361	ProLeuTyrAlaAsnValHisHisGlnLysGlyLysAspGluGlyValValTyrSerVal	380
Db	1167	CCACTATATGCCAACGTGCATCACCAGAAAGGGAAAGATGAAGGTGTTGTCTACTCTGTG	1226
Qy	381	ValHisArgThrSerLysArgSerGluAlaArgSerAlaGluPheThrVal-GlyArgLy	400
Db	1227	GTGCATAGAACCTCAAAGAGGAGTGAAGCCAGGTCTGCTGAGTTCACCGTGGGGA-----	1281
Qy	400	sAspSerSerIleIleCysAlaGluValArgCysLeuGlnProSerGluValSerSerTh	420
		:::	
Db	1282	-GAAAGTTCTATCATCTGTGCGAGGTGAGATGCCTGCAGCCAGTGAGGTTTCATCCAC	1340
Qy	420	rGluValAsnMetArgSerArgThrLeuGlnGluProLeuSerAspCysGluGluValLe	440
Db	1341	GGAGGTGAATATGAGAAGCAGGACTCTCCAAGAACCCTTAGCGACTGTGAGGAGTTCT	1400
Qy	440	uCys	441
Db	1401	CTGC	1404

RESULT 6

AK131201

LOCUS AK131201 1997 bp mRNA linear PRI 09-JAN-2008